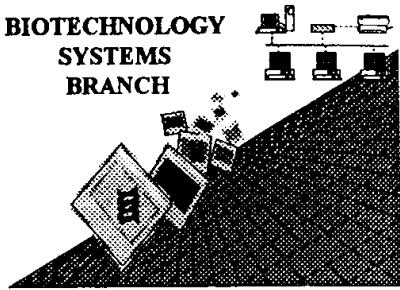


K. Schnizer

# RAW SEQUENCE LISTING

## ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



### **FILE COPY**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/247,874

Art Unit / Team No.: 1632

Date Processed by STIC: 6/15/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED    SUGGESTED CORRECTION

SERIAL NUMBER: 09/247,874

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1  Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2  Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3  Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4  Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5  Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6  Variable Length Sequence(s)  contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7  PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8  Skipped Sequences (OLD RULES) Sequence(s)  missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")**  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
**This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9  Skipped Sequences (NEW RULES) Sequence(s)  missing. If intentional, please use the following format for each skipped sequence.  
**<210> sequence id number**  
**<400> sequence id number**  
**000**
- 10  Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11  Use of <213>Organism (NEW RULES) Sequence(s)  are missing this mandatory field or its response.
- 12  Use of <220>Feature (NEW RULES) Sequence(s)  are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13  PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/247,874**

DATE: 06/15/1999  
 TIME: 11:56:38

Input Set: I247874.RAW

**This Raw Listing contains the General Information Section and up to first 5 pages.**

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 2 di Giovine, Francesco Saverio  
 3 <120> TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC BASED ON A NOVEL IL-1B  
 4 MUTATION  
 5 <130> FILE REFERENCE: MSA-004.01  
 6 <140> CURRENT APPLICATION NUMBER: US/09/247,874  
 7 <141> CURRENT FILING DATE: 1999-02-10  
 8 <160> NUMBER OF SEQ ID NOS: 18  
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 189 tcagaaggct gcttggagag caagtccatg aaatgctttt tttccacag tagaacctat 420  
 190 ttccctcggt tctcaaatac ttgcacagag gctcaactccc ttggataatg cagagcgagc 480  
 191 acgataacctg gcacatacta atttgaataa aatgctgtca aattcccatc caccatcca 540  
 192 agcagcaaac tctatctcac ctgaatgtac atgccaggca ctgtgttaga cttggctcaa 600  
 193 aaagatttca gtttccctgga ggaaccagga gggcaagggtt tcaactcagt gctataagaa 660  
 194 gtgttacagg ctggacacgg tggctcacgc ctgtatccc aacatttggg aggccgaggc 720

W--&gt;

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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/247,874**

DATE: 06/15/1999  
 TIME: 11:56:38

Input Set: I247874.RAW

```

195      gggcagatca caaggtcagg agatcgagac catcctggct aacatggtga aaccctgtct 780
196      ctactaaaaa tacaaaaaaat tagccgggcg ttggcggcag gtgcctgttag tcccagctgc 840
197      tggggaggct gaggcaggag aatggtgtga acccgggagg cggaacctgc aggggggccga 900
198      gatcgtgcca ctgcactcca gcctggcga cagagtgaga ctctgtctca aaaaaaaaaa 960
199      aaaagtgtta tcatgcagac ctgtcaaaga ggc当地aggag ggtgttctca cactccagc 1020
200      actgttcata acctggactc tcattcattc tacaaatgga gggctcccct gggcagatcc 1080
201      ctggagcagg cactttctg gtgtctcggt taaagagaaa ctgataactc ttggtattac 1140
202      caagagatag agtctcagat ggatattctt acagaaaacaa tattccact tttcagagtt 1200
203      caccaaaaaa tcattttagg cagagctcat ctggcattga tctgggtcat ccatgagatt 1260
204      ggcttagggta acagcacctg gtcttgagg gttgtgttag cttatctcca ggggttgc(cc) 1320
205      aactccgtca ggagcctgaa ccctgcatac cgtatgttct ctgccccagc caagaaaaggt 1380
206      caatttctc ctcagaggct cctgcaattt acagagagct cccgaggcag agaacagcac 1440
207      ccaaggtaga gaccacaccc ctcaatacag acagggaggg ctattggccc ttcattgtac 1500
208      ccattttatcc atctgttaatg gggagattc ctaaacttaa gtacaaagaa gtgaatgaag 1560
209      aaaagtatgt gcatgtataa atctgtgtgt ctccacttt gtcccacata tactaaattt 1620
210      aaacattttt ctaacgtggg aaaatccagt attttaatgt ggacatcaac tgcacaacga 1680
211      ttgtcagggaa aacaatgtcat atttgcattt tgatacattt gcaaaatgtg tcatagttt 1740
212      ctactccctt cccttccatg aaccagagaa ttatctcagt ttattagtcc cctccctaa 1800
213      gaagcttcca ccaataactct ttccctt cctttaactt gattgtgaaa tcaggtattc 1860
214      aacagagaaa ttctcagcc tcctacttctt gcttttgaaa gctataaaaaa cagcgaggga 1920
215      gaaactggca gataccaaac ctcttcgagg cacaaggcac aacaggctgc tctgggattc 1980
216      tcttcagcca atcttcattt ctcaagtatg actttaatct tccttacaac taggtgctaa 2040
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218      tcttcctctg tcttcctctc ccttcctctc tgccctctctc otcagcttt tgcaaaaaatg 2160
219      ccaggtgtaa tataatgttt atgactcgaa aaatattctg ggaatggata ctgcttatct 2220
220      aacagctgac accctaaagg ttagtgtcaa agcctctgct ccagctctcc tagccaataac 2280
221      attgctagtt ggggtttggg ttagcaatgt ctttctcta gacccaaagg acttctcttt 2340
222      cacacattca ttcatattact cagagatcat ttctttgcat gactgccatg cactggatgc 2400
223      tgagagaaaat cacacatgaa cgtagccgtc atggggaaatg cactcattt ctcctttta 2460
224      cacaggtgtc tgaaggcagcc atggcagaag tacctgagct cgccagtgaa atgatggctt 2520
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226      agagtgttat ctgtgtttgg agaccagatt ttccctttaa attgctctt tcagtgccaa 2640
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228      tgggacctgg aggctatcca gatgtttgt tgcaagggtc tcctgcagag gcaaatgggg 2760
229      agaaaagatt ccaagcccac aataacaagga atccctttgc aaagtgtggc ttggaggag 2820
230      agggagagct cagatttttag ctgactctgc tgggcttagag gttagcctc aagatccaac 2880
231      agggagcacc agggtgc(cc) cctgcccaggc ctagaatctg ccttcggac tttctgcgc 2940
232      atatcactgt gaaacttgcg aggtgtttca ggcagctttt agaggcaggc tttttgcagt 3000
233      ttcttattgaa cagtcagtc ttgtacacag ggaaggaaaa ataaacctgt ttagaagaca 3060
234      taatttgagac atgtccctgt ttttattaca gtggcaatga ggtacttgc ttctttgaag 3120
235      ctgtatggccc taaaacagatg aaggtaaagac tatgggtta actcccaacc caaggaagg 3180
236      ctcttaacaca gggaaagctc aaagaaggga gttctggcc actttgatgc catgttattt 3240
237      tgtttttagaa agactttaaatc ctcttcagt gagacacagg ctgcaccact tgctgacctg 3300
238      gccactttgtt catcatatca ccacagtcac tcactaacgt tgggtgtggt ggccacactt 3360
239      ggtggtgaca ggggaggagt agtgataatg ttcccttttc atagtaggaa gacaaccaag 3420
240      tcttcacat aaatttgatt atccctttaa gagatggatt cagcctatgc caatcactt 3480
241      agttaaactc tgaacccaag agatgatctt gagaactaac atatgtctac cccttttgag 3540
242      tagaatagtt ttttgcattc tgggggtggaa ctataacaa caagacatag atgatataaa 3600
243      caaaaagatg aatttgagact tggaaagaaaa ccattcactt gctgttgcac tttgacaatg 3660
244      cattttaccc gctttggacc tcatactgaaa aataaaaggcc tgagctggat gatctctgag 3720

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY  
PATENT APPLICATION US/09/247,874

DATE: 06/15/1999

TIME: 11:56:38

Input Set: I247874.RAW

Line ? Error/Warning

Original Text

17 W "N" or "Xaa" used: Feature required  
185 W "N" or "Xaa" used: Feature required  
437 W "N" or "Xaa" used: Feature required

atcctgtgga ggcanncaga ggagtcccct aggccacc  
atcctgtgga ggcanncaga ggagtcccct aggccacc  
ccgactcgag nnnnnnatgt gg